```
=> fil reg; d que l4; d que l5; d que l2
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n = 11

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L4             0 SEA FILE=REGISTRY ABB=ON  C[-C][-C][-C]CCCCCCCCCC[-C]C[-C][-C]
                  [-C]C/SQSP
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n = 14 exact sequence

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L5             0 SEA FILE=REGISTRY ABB=ON  ^C[-C][-C][-C]C[-C]C[-C][-C][-C]C^/SQ
                  SP
```

n = 1 embedded w/in a larger sequence

```
L2          1615 SEA FILE=REGISTRY ABB=ON  C[-C][-C][-C]C[-C]C[-C][-C][-C]C/SQSP
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=> fil capl; s l2
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FILE LAST UPDATED: 8 Aug 2004  (20040808/ED)

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L6 531 L2

=> sort l6 py a 1-
SORT IS APPROXIMATELY 81% COMPLETE
PROCESSING COMPLETED FOR L6
L9 531 SORT L6 1- PY A

sorted answer set by publication year

=> d ibib ab hitrn l9 1-30

printed 30 oldest references

L9 ANSWER 1 OF 531 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1985:536288 CAPLUS
DOCUMENT NUMBER: 103:136288
TITLE: Sea urchin metallothionein sequence: Key to an evolutionary diversity
AUTHOR(S): Nemer, Martin; Wilkinson, David G.; Travaglini, Elizabeth C.; Sternberg, Edmund J.; Butt, Tauseef R.
CORPORATE SOURCE: Fox Chase Cancer Cent., Inst. Cancer Res., Philadelphia, PA, 19111, USA
SOURCE: Proceedings of the National Academy of Sciences of the United States of America (1985), 82(15), 4992-4
DOCUMENT TYPE: CODEN: PNASA6; ISSN: 0027-8424
LANGUAGE: Journal
English

AB The metallothioneins (MTs) constitute a diverse family of proteins, which are enriched in cysteines and bind heavy metals. The amino acid sequence of sea urchin MT was obtained from its mRNA sequence and compared with MT sequences of various sources. A largely conserved sequence of 10 amino acids, the central segment, is located near the center of the MT mols. of Neurospora, yeast, and Drosophila and the center of putative domains in mammalian and sea urchin MTs. The sea urchin C-terminal-half MT resembles the mammalian 9-cysteine N-terminal MT domain I, both in the presence of this central segment and in the relative placement of cysteine residues. Conversely, the sea urchin N-terminal-half MT, contg. 11 cysteines, resembles the mammalian C-terminal MT domain II in its exclusive enrichment in vicinal cysteines. The reversed order of these sea urchin and mammalian MT halves appears to be just 1 aspect of a diversity based on the elaboration of structures contg. the central segment. Still another variation in this diversity is the duplication of the central segment, apparent in Drosophila and crab MTs.

IT **98513-00-9**
RL: PRP (Properties)
(amino acid sequence of)

use Registry # to match citation to sequence (printed at end of search)

L9 ANSWER 2 OF 531 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1988:217090 CAPLUS
DOCUMENT NUMBER: 108:217090
TITLE: Sequence of pTOM5, a ripening-related cDNA from tomato
AUTHOR(S): Ray, John; Bird, Colin; Maunders, Martin; Grierson, Don; Schuch, Wolfgang
CORPORATE SOURCE: Plant Biotechnol. Group, ICI, Runcorn/Cheshire, WA7 4QE, UK
SOURCE: Nucleic Acids Research (1987), 15(24), 10587
DOCUMENT TYPE: CODEN: NARHAD; ISSN: 0305-1048
LANGUAGE: Journal
English

AB The nucleotide sequence of pTOM5, a cDNA clone coding for an mRNA that accumulates during ripening of tomato fruit, was detd. This cDNA codes for a polygalacturonase of 46.7 daltons mol. wt.

IT **114541-20-7**

Searched by Barb O'Bryen, STIC 2-2518

RL: PRP (Properties)
(amino acid sequence of)

L9 ANSWER 3 OF 531 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1988:1367 CAPLUS
DOCUMENT NUMBER: 108:1367
TITLE: Post-transcriptional restriction of gene expression in sea urchin interspecies hybrid embryos
AUTHOR(S): Conlon, Ronald A.; Tufaro, Frank; Brandhorst, Bruce P.
CORPORATE SOURCE: Dep. Biol., McGill Univ., Montreal, QC, H3A 1B1, Can.
SOURCE: Genes & Development (1987), 1(4), 337-46
CODEN: GEDEEP; ISSN: 0890-9369
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The synthesis of many paternal species-specific proteins is reduced in all stages of sea urchin interspecies hybrid embryos, due to the reduced amts. of some paternal mRNA species in hybrid embryos compared with the embryos of the paternal species. Possible explanations for this restriction were tested. Cloned cDNAs were selected that were specific for paternal RNA sequences having reduced amts. (to 2-20% of normal) in hybrid embryos derived from a cross of Strongylocentrotus purpuratus eggs with Lytechinus pictus sperm. Several of these RNA species are barely detectable in the eggs, but they accumulate extensively (5- to 40-fold) during L. pictus embryongenesis. Thus, the restricted expression of these paternal genes in hybrid embryos is not the result of the persistence of stable maternal mRNA species stored in eggs and not replaced by zygotic transcription. The accumulation of some of these L. pictus transcripts is also reduced in the reciprocal cross (L. pictus eggs .times. S. purpuratus sperm); therefore, the full expression of these L. pictus genes in hybrid embryos is not dependent on species-specific maternal factors stored in the egg. The transcriptional activity of one such gene was estd. using a run-on assay in isolated nuclei; it is as actively transcribed in hybrid as it is in homospecific embryos, but in hybrid embryos the cytoplasmic transcript accumulates to only 2-15% of the normal level. Sequence anal. indicates that this gene encodes a metallothionein. Mechanisms are discussed that might account for the post-transcriptional restriction of expression of some genes in hybrid embryos.
IT **111694-22-5**
RL: PRP (Properties)
(amino acid sequence of)

L9 ANSWER 4 OF 531 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1987:528213 CAPLUS
DOCUMENT NUMBER: 107:128213
TITLE: Metallothionein genes in Drosophila melanogaster constitute a dual system
AUTHOR(S): Mokdad, Raja; Debec, Alain; Wegnez, Maurice
CORPORATE SOURCE: Cent. Genet. Mol., Cent. Natl. Rech. Sci., Gif-sur-Yvette, 91190, Fr.
SOURCE: Proceedings of the National Academy of Sciences of the United States of America (1987), 84(9), 2658-62
CODEN: PNASA6; ISSN: 0027-8424
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A metallothionein (MT) cDNA clone was selected from a cadmium-resistant D. melanogaster cell line and sequenced. This clone includes an open reading frame coding for a 43-amino acid protein whose characteristics are a high cysteine content (12 cysteines, 28% of all residues) and a lack of arom. amino acids. This protein differs markedly from the Drosophila MT (Mtn gene) previously reported (Lastowski-Perry, D., et. al., 1985). Thus, the MT system of Drosophila consists of at least two distantly related genes, in sharp contrast with vertebrate MT systems, in which the different

members of MT gene families display high similarity. The gene corresponding to this MT cDNA (Mto) is inducible in Drosophila cell lines and in both larval and adult flies.

IT **109189-62-0**
RL: PRP (Properties)
(amino acid sequence of)

L9 ANSWER 5 OF 531 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1987:114478 CAPLUS
DOCUMENT NUMBER: 106:114478
TITLE: Metallothionein genes MTa and MTb expressed under distinct quantitative and tissue-specific regulation in sea urchin embryos
AUTHOR(S): Wilkinson, David G.; Nemer, Martin
CORPORATE SOURCE: Inst. Cancer Res., Fox Chase Cancer Cent., Philadelphia, PA, 19111, USA
SOURCE: Molecular and Cellular Biology (1987), 7(1), 48-58
CODEN: MCEBD4; ISSN: 0270-7306
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Sea urchin (Strongylocentrotus purpuratus) embryo metallothionein (MT) mRNAs MTa and MTb have distinct cDNA sequences and are transcripts of different genes of a multigene family. These MT mRNAs differ in size and in their 3'-untranslated sequences. They encode proteins that are unusual among MT isotypes in that the relative positions of their cysteine residues are partially out of register, suggesting potential differences in function. In pluteus larvae MTa mRNA is expressed abundantly and exclusively in the ectoderm, while MTb mRNA, which is restricted to the endomesoderm at a low endogenous level, can be induced to a high level by heavy metal ions (M2+). MT expression in the embryo, which is at a much higher level than in the egg, requires M2+ for gene transcription, is developmentally regulated, and is >90% MTa mRNA. When induced by added M2+, however, MTa and MTb mRNAs accumulate to almost equal levels. The differences in the ratios of MTa/MTb expressed endogenously and inductively are not attributable to differences in the stabilities of these MT mRNAs, which were obsd. under conditions of M2+ depletion, or in their inducibilities, which were obsd. at moderate to high M2+ levels. The MTa gene responds to M2+ at a lower threshold level than MTb, so that at very low M2+ concns. the ratio of induced MTa/MTb mRNA is high and equiv. to the endogenous ratio. Thus, endogenous expression of the MTa gene is selectively enhanced in the ectoderm by determinants that are responsive at low M2+ threshold concns.

IT **107248-70-4**
RL: PRP (Properties)
(amino acid sequence of)

L9 ANSWER 6 OF 531 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1988:217053 CAPLUS
DOCUMENT NUMBER: 108:217053
TITLE: DNA sequence of the HPV-16 E5 ORF and the structural conservation of its encoded protein
AUTHOR(S): Bubb, Vivien; McCance, Dennis J.; Schlegel, Richard
CORPORATE SOURCE: Lab. Tumor Virus Biol., Natl. Cancer Inst., Bethesda, MD, 20892, USA
SOURCE: Virology (1988), 163(1), 243-6
CODEN: VIRLAX; ISSN: 0042-6822
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Infection of cervical epithelium by human papillomavirus type 16 (HPV-16) appears to be closely assocd. with the development of cervical dysplasia and carcinoma. By inference from genetic and biochem. studies of the bovine papillomavirus, the E5 open reading frame (ORF) of the human

papillomaviruses is anticipated to encode a transforming protein. In an effort to compare the E5 ORF of HPV-16 with other human papillomaviruses and bovine papillomavirus, this region was sequenced from a new isolate of HPV-16 which was derived from extrachromosomal viral DNA within a premalignant cervical lesion (cervical intraepithelial neoplasia, grade III, or CIN III). In addn., the original isolate of HPV-16 was also sequenced. Both HPV-16 isolates contained and addnl. nucleotide (T) at bp 3906. This nucleotide addn. caused a frameshift in the E5 ORF such that it now contains an initiation codon at bp 3849; the frameshift also alters the predicted E5 NH2 terminus but retains the original COOH half of the protein. E5 proteins encoded by several HPVs which infect the genital region (e.g., types 6, 11, 16, 18, 33) exhibit a conserved trimodal hydrophobic structure, but not a conserved amino acid sequence.

IT **114572-74-6**
RL: PRP (Properties)
(amino acid sequence of)

L9 ANSWER 7 OF 531 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1990:453358 CAPLUS
DOCUMENT NUMBER: 113:53358
TITLE: Structure of ectodermally expressed sea urchin metallothionein gene and characterization of its metal-responsive region
AUTHOR(S): Harlow, Patricia; Watkins, Elizabeth; Thornton, Ruth D.; Nemer, Martin
CORPORATE SOURCE: Fox Chase Cancer Cent., Inst. Cancer Res., Philadelphia, PA, 19111, USA
SOURCE: Molecular and Cellular Biology (1989), 9(12), 5445-55
CODEN: MCEBD4; ISSN: 0270-7306
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The metallothionein-A gene in the metallothionein gene family of the sea urchin Strongylocentrotus purpuratus (SpMTA gene) was sequenced and found to contain three coding exons plus a 3' entirely noncoding exon. Putative .alpha. and .beta. MT domains were encoded, by exons 2 and 3, resp., in reverse of the order in vertebrate metallothionein genes. The SpMTA promoter was characterized by expression of recombinant constructs contg. various portions of the proximal 678-base-pair (bp) 5'-flanking region of the SpMTA gene. Zygotes injected with constructs were cultured to the blastula stage in the presence of a heavy-metal chelator and then incubated in the presence or absence of cadmium. The longest constructs were expressed only when heavy-metal ion was present. Two putative metal-responsive elements (MREs a and b) within 240 bp of the transcription start site resembled mammalian MREs in their crit. 8-bp cores (TGCRCNCS) and in their locations relative to each other and to the TATA box. Elimination of activity by site-specific mutations in MREs a and b, sep. or in both, identified them as metal regulatory elements. Thus, MRE recognition in this invertebrate resembles that in vertebrates. Upstream sites with single-mismatched MREs neither acted as MREs nor amplified the activity of MREs a and b. The SpMTA, Spe1, and CyIIIa actin genes, which have the same ectodermal specificity, have common DNA elements at relatively similar locations in their promoter regions; however, these elements are insufficient in themselves to promote gene expression.

IT **98513-00-9**, Metallothionein (Strongylocentrotus purpuratus protein moiety reduced) **128392-65-4**, Metallothionein (Strongylocentrotus purpuratus clone .lambda.MT206 protein moiety reduced)
RL: PRP (Properties)
(amino acid sequence of)

L9 ANSWER 8 OF 531 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1990:113291 CAPLUS

DOCUMENT NUMBER: 112:113291
TITLE: Candida glabrata metallothioneins. Cloning and sequence of the genes and characterization of proteins
AUTHOR(S): Mehra, Rajesh K.; Garey, James R.; Butt, Tauseef R.; Gray, William R.; Winge, Dennis R.
CORPORATE SOURCE: Med. Cent., Univ. Utah, Salt Lake City, UT, 84132, USA
SOURCE: Journal of Biological Chemistry (1989), 264(33), 19747-53
CODEN: JBCHA3; ISSN: 0021-9258
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Southern blot anal. has identified several metallothionein gene sequences in a human pathogenic yeast C. glabrata. Two of these genes encoding proteins designated MT-I and MT-II have been cloned and sequenced. No introns were found in either of the genes. The complete primary structure of MT-II was also detd. by protein sequencing methods. As isolated, MT-I and MT-II consist of 62 and 51 amino acids, resp. The only residues predicted from the nucleotide sequence but not present in the isolated protein are the amino-terminal methionines in each sequence. MT-I contains 18 cysteines, 14 of which are present as Cyx-X-Cys motifs and two addnl. cysteines in a Cys-X-X-Cys sequence. The sequence of MT-II contains 16 cysteinyl residues, 14 of which are in Cys-X-Cys sequences. Fluorescence spectroscopy indicates the presence of Cu(I)-thiolate bonds in both proteins. The binding stoichiometries are 11-12 for MT-I and 10 for MT-II. Under certain nutritional conditions, a truncated form of MT-II was also produced. Northern anal. of the total cellular RNA from copper-treated cells showed that both MT-I and MT-II genes are regulated by this metal ion in a concn.-dependent fashion. The concns. of MT-II mRNA appeared to be higher than that of MT-I mRNA at all concns. of copper sulfate tested. Both genes are inducible by silver but not by cadmium salts. Cadmium ions, however, are effective in reducing the control levels of both MT-I and MT-II mRNAs.

IT **125691-65-8**, Metallothionein I (Candida glabrata strain 67 protein moiety reduced)
RL: PRP (Properties)
(amino acid sequence of)

L9 ANSWER 9 OF 531 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1991:137042 CAPLUS
DOCUMENT NUMBER: 114:137042
TITLE: Metallothionein Mto gene of Drosophila melanogaster: structure and regulation
AUTHOR(S): Silar, Philippe; Theodore, Laurent; Mokdad, Raja; Erraiss, Nour Eddine; Cadic, Agnes; Wegnez, Maurice
CORPORATE SOURCE: Lab. Embryol. Mol., Univ. Paris XI, Orsay, 91405, Fr.
SOURCE: Journal of Molecular Biology (1990), 215(2), 217-24
CODEN: JMOBAK; ISSN: 0022-2836
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The sequence of the Mto gene, one of the 2 known metallothionein geens of D. melanogaster, is reported and compared with that of the other metallothionein gene, Mtn. The main structural features are the presence of a small intron (61 bp), the presence of 4 potential MREs (metal regulatory elements) and the absence of a TATA box in the promoter region. Of all metals tested, Hg2+, Cd2+ and Cu2+ are the most efficient ions for inducing an increase in Mto gene transcription. The Mto and Mtn genes are differentially regulated during normal development. Transcription of Mto is detected early in embryogenesis (0 to 3 h) and persists to the third larval instar, while Mtn expression starts later in embryogenesis (12 to 15 h) and is thereafter maintained throughout larval development and adult stages. Sequencing of the Mto protein is in good agreement with the nucleic acid data. Surprisingly, attempts to isolate and characterize the

Mtn protein were unsuccessful. Several lines of evidence suggest that this metallothionein is rapidly incorporated after its synthesis into lysosomes, where it would be processed in a way that would not permit its purifn. The function of the Mtn protein thus appears to be mainly related to detoxification processes. The pattern of expression of Mto suggests that this gene may be involved in the control of metal homeostasis during development.

IT **109189-62-0**, Metallothionein (Drosophila melanogaster clone pCd2/pCd14 protein moiety reduced)
RL: PRP (Properties)
(amino acid sequence of)

L9 ANSWER 10 OF 531 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1990:492286 CAPLUS
DOCUMENT NUMBER: 113:92286
TITLE: Metallothionein genes from the flowering plant Mimulus guttatus
AUTHOR(S): De Miranda, J. R.; Thomas, M. A.; Thurman, D. A.; Tomsett, A. B.
CORPORATE SOURCE: Dep. Genet. Microbiol., Univ. Liverpool, Liverpool, L69 3BX, UK
SOURCE: FEBS Letters (1990), 260(2), 277-80
CODEN: FEBLAL; ISSN: 0014-5793
DOCUMENT TYPE: Journal
LANGUAGE: English

AB In response to excess metal, high plants produce metal-binding peptides ([.gamma.EC]nG) whose biosynthesis is believed to be mediated by enzymes involved in glutathione (.gamma.ECG) metab. In contrast, animals synthesize metallothioneins: low mol. wt., cysteine-rich, metal-binding proteins. In an investigation of copper-regulated genes in the copper-tolerant flowering plant M. guttatus, a series of cDNA clones for 2 genes which encode a protein with class I metallothionein domains were isolated. This represents the first description of a metallothionein gene in a flowering plant.

IT **128825-82-1**, Metallothionein (Mimulus guttatus clone J49 protein moiety reduced)
RL: PRP (Properties)
(amino acid sequence of)

L9 ANSWER 11 OF 531 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1990:453446 CAPLUS
DOCUMENT NUMBER: 113:53446
TITLE: A gene from pea (Pisum sativum L.) with homology to metallothionein genes
AUTHOR(S): Evans, I. Marta; Gatehouse, Laurence N.; Gatehouse, John A.; Robinson, Nigel J.; Croy, Ronald R. D.
CORPORATE SOURCE: Dep. Biol. Sci., Univ. Durham, Durham, DH1 3LE, UK
SOURCE: FEBS Letters (1990), 262(1), 29-32
CODEN: FEBLAL; ISSN: 0014-5793
DOCUMENT TYPE: Journal
LANGUAGE: English

AB While searching for organ-specific genes in pea, the authors isolated a gene (designated PsMTA) which has an ORF encoding a predicted protein with some similarity to metallothioneins. The PsMTA transcript is abundant in roots which have not been exposed to elevated concns. of trace metals.

IT **128392-85-8**, Metallothionein (pea strain Feltham First gene PsMTA protein moiety reduced)
RL: PRP (Properties)
(amino acid sequence of)

L9 ANSWER 12 OF 531 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1993:141989 CAPLUS

DOCUMENT NUMBER: 118:141989
TITLE: A plant metallothionein produced in E. coli
AUTHOR(S): Kille, Peter; Winge, Dennis R.; Harwood, John L.; Kay, John
CORPORATE SOURCE: Dep. Biochem., Univ. Wales Coll. Cardiff, Cardiff, CF1 1ST, UK
SOURCE: FEBS Letters (1991), 295(1-3), 171-5
CODEN: FEBLAL; ISSN: 0014-5793
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A metallothionein cDNA was generated from pea (Pisum sativum) roots, amplified by PCR and inserted into a plasmid for expression in Escherichia coli. Purifn. of the resultant product generated 3 pools of cadmium-contg. material after DEAE-cellulose chromatog. The amino acid compn. of each was in excellent agreement with that predicted for pea metallothionein. A cadmium content of .apprx.6 g.atoms per mol of protein was estd. N-terminal sequence anal. revealed that the recombinant mol. had been proteolyzed within the extended region linking the 2 cysteine-rich (putative) metal-binding regions. The significance of these findings in terms of the protein folding/targeting of the mol. are considered.

IT **128392-85-8**, Metallothionein (pea gene PsMTA protein moiety reduced)
RL: PRP (Properties)
(amino acid sequence of, complete)

L9 ANSWER 13 OF 531 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1992:627755 CAPLUS
DOCUMENT NUMBER: 117:227755
TITLE: Copper-inducible expression system for heterologous genes in Saccharomyces
INVENTOR(S): Macreadie, Ian Geoffrey; Vaughan, Paul Richard; Azad, Ahmed Abdullah
PATENT ASSIGNEE(S): Commonwealth Scientific and Industrial Research Organisation, Australia
SOURCE: Pat. Specif. (Aust.), 40 pp.
CODEN: ALXXAP
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
AU 614959	B2	19910919	AU 1988-15845	19880506
AU 8815845	A1	19881110		
PRIORITY APPLN. INFO.:			AU 1987-1788	19870507

AB The use of the CUP1 gene to achieve high-level expression of heterologous genes in Saccharomyces cerevisiae is described. Expression is driven by the Cu-inducible promoter, and Cu resistance is conferred by accumulation of the metallothionein. The metallothionein remains able to confer Cu resistance even when it is part of a fusion protein with a much larger protein. The expression cassette includes a multi-cloning site. The construction of the expression cassettes by std. methods and the Cu-inducible expression of a no. of heterologous genes in S. cerevisiae is demonstrated. The expression cassette functions constitutively in Schizosaccharomyces pombe.

IT **134801-80-2**, Metallothionein (Saccharomyces cerevisiae strain MW3070-8B gene CUP1 protein moiety reduced)
RL: USES (Uses)
(gene for, in prepn. copper-inducible expression cassette for heterologous gene expression in yeast)

L9 ANSWER 14 OF 531 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1992:585821 CAPLUS
DOCUMENT NUMBER: 117:185821
TITLE: Primary structure of a novel barley gene differentially expressed in immature aleurone layers
AUTHOR(S): Klemsdal, Sonja S.; Hughes, Wayne; Loenneborg, Anders; Aalen, Reidunn B.; Olsen, Odd Arne
CORPORATE SOURCE: Plant Mol. Biol. Lab., NLVF, Aas, 1432, Norway
SOURCE: Molecular and General Genetics (1991), 228(1-2), 9-16
CODEN: MGGEAE; ISSN: 0026-8925
DOCUMENT TYPE: Journal
LANGUAGE: English
AB As a direct approach to elucidate the mol. biol. of barley aleurone cell development, an aleurone cDNA library made from poly(A)+ RNA of immature grains was differently screened for clones representing transcripts present in the aleurone but not in the starchy endosperm. For one of these clones, B22E, which hydridies to a 0.7 kb transcript, Northern and in situ hybridization revealed that expression is under complex spatial, temporal, and hormonal control in barley grains. CDNAs corresponding to B22E transcripts were isolated from aleurone/pericarp and embryo of developing grains, and from germinating scutella. Among these were the nearly full-length aleurone/pericarp clone pB22E.a16 (541 bp). CDNAs matching the sequence of this clone (type 1 transcript) were found for all tissues investigated. In addn., cDNAs with an extra 12 bp insertion (type 2 transcript) were obtained from germinating scutella. The 2 different transcripts can encode novel barley proteins of 115 and 119 amino acids, resp. A gene designated B22EL8 was isolated and sequenced; it encodes the type 1 B22E transcript and contains 2 introns of 145 and 125 bp. Particle bombardment of barley aleurone with a B22EL8 promoter-GUS (.beta.-glucuronidase) construct demonstrates that the promoter (3 kb) is active in developing barley grains. The promoter is not, however, active in the seeds of tobacco plants transgenic for the B22EL8 gene, indicating the existence of sequences specific for monocots. A comparison of 1.4 kb of upstream sequence of B22E with the maize c1 promoter reveals a no. of short, identical sequences which may be responsible for aleurone cell-specific gene transcription.
IT **143972-11-6**, Protein (barley clone pB22EL8 gene B22EL8 reduced)
143972-14-9, Protein (barley clone pB22E.g49 gene B22EL8 reduced)
143972-16-1, Protein (barley clone pB22E.g411/pB22E.g312/pB22E.g1 gene B22E reduced)
RL: PRP (Properties)
(amino acid sequence of)

L9 ANSWER 15 OF 531 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1992:52644 CAPLUS
DOCUMENT NUMBER: 116:52644
TITLE: A metallothionein-like gene from maize (Zea mays). Cloning and characterization
AUTHOR(S): De Framond, Annick J.
CORPORATE SOURCE: Dep. Plant Mol. Biol., CIBA-Geigy, Research Triangle Park, NC, 27709-2257, USA
SOURCE: FEBS Letters (1991), 290(1-2), 103-6
CODEN: FEBLAL; ISSN: 0014-5793
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A differentially expressed maize gene has been cloned and sequenced. Transcriptional and translational start sites have been mapped and 2.5 kb of 5' flanking DNA were sequenced. The 8 kDa protein encoded by this gene shows striking similarity to the metallothionein-like proteins recently described in Pisum sativum and Mimulus guttatus. The maize MT-L gene message is very abundant in roots without exposure to high levels of

metals, present at lower concn. in leaves and pith, and at very low concn. in seed.

IT **138672-78-3**, Protein (corn clone pCIB1324 7.48-kilodalton reduced)
RL: PRP (Properties)
(amino acid sequence of)

L9 ANSWER 16 OF 531 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1992:52640 CAPLUS
DOCUMENT NUMBER: 116:52640
TITLE: An iron deficiency-specific cDNA from barley roots having two homologous cysteine-rich MT domains
AUTHOR(S): Okumura, Nami; Kishi Nishizawa, Naoko; Umehara, Yosuke; Mori, Satoshi
CORPORATE SOURCE: Lab. Plant Nutr. Fert., Univ. Tokyo, Tokyo, 113, Japan
SOURCE: Plant Molecular Biology (1991), 17(3), 531-3
CODEN: PMBIDB; ISSN: 0167-4412
DOCUMENT TYPE: Journal
LANGUAGE: English

AB An attempt was made to isolate and characterize cDNA clones involved in iron acquisition, i.e. the genes of mugineic acid-family phytosiderophores (MAs) biosynthesis and also the Fe(III)-MAs transporter. These proteins or enzymes have neither been identified nor isolated to date. First, a .lambda.gt10 cDNA library was constructed with mRNA isolated from Fe-deficient barley roots. Then the library was differentially screened between cDNA probes from mRNA of Fe-deficient nd Fe-sufficient barley roots. Altogether, seven cDNA clones which hybridized specifically to a probe of Fe-deficient barley roots were selected. Their inserts were subcloned and then DNAs were sequenced. The longest clone of about 500 bp was assumed to have the full length by northern hybridization. We named this clone ids-1 (deficiency-specific clone 1). The sequenced ids-1 is composed of 503 nucleotides, a putative open reading frame of 222 bp, a 5'-untranslated sequence of 31 bp and a 3'-noncoding region of 250 bp. A 3'-noncoding region contains the sequence AATATA 23 bp upstream from the polyadenylation site which is homologous to polyadenylation signals (AATAAA). There are many sequences of palindrome, hairpin loop and tandem repeats. The putative open reading frame encodes a protein of 74 residues (7500 Da) which contains two cysteine-rich regions. The strong similarity of the ids-1 sequence to animal and fungal (metallothioneins) MTs is in two domains. Each domain contains six cysteines arranged as Cys-X-Cys clusters, a presumable constraint of metal-binding characteristic of MTs.

IT **138672-77-2**, Protein (barley clone ids-1 7.46-kilodalton reduced)
RL: PRP (Properties)
(amino acid sequence of)

L9 ANSWER 17 OF 531 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1991:672709 CAPLUS
DOCUMENT NUMBER: 115:272709
TITLE: Root-specific promoter from maize
INVENTOR(S): De Framond, Annick J.
PATENT ASSIGNEE(S): Ciba-Geigy A.-G., Switz.
SOURCE: Eur. Pat. Appl., 32 pp.
CODEN: EPXXDW
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 452269	A2	19911016	EP 1991-810247	19910404
EP 452269	A3	19920916		
EP 452269	B1	20021009		

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE

AT 225853	E	20021015	AT 1991-810247	19910404
ES 2187497	T3	20030616	ES 1991-810247	19910404
US 5466785	A	19951114	US 1994-322962	19941013
US 5792925	A	19980811	US 1995-450653	19950525
PRIORITY APPLN. INFO.:			US 1990-508207 A	19900412
			US 1993-71209 B1	19930602
			US 1994-322962 A3	19941013

AB A cDNA and gene for a transcript that is expressed in roots of Zea mays but not in seed are cloned and characterized for use in tissue-specific gene expression in transgenic plants. The cDNA was cloned from a root cDNA bank in pUC9 by differential screening with root and seed cDNA probes. The genomic clone was then isolated and shown to be single-copy. Sequence comparisons showed the encoded protein to be very similar to pea metallothioneins. The 5'-flanking region of the genomic clone (2.5 kilobases) was able to drive expression of a reporter gene in tobacco with some specificity for root tissue.

IT **138672-78-3**, Metallothionein (corn clone pCIB1325 protein moiety reduced)
RL: PRP (Properties)
(amino acid sequence of and root-specific expression of gene for)

L9 ANSWER 18 OF 531 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER:	1991:672115 CAPLUS
DOCUMENT NUMBER:	115:272115
TITLE:	Isolation of a gene for a metallothionein-like protein from soybean
AUTHOR(S):	Kawashima, Ichiro; Inokuchi, Yoshio; Chino, Mitsuo; Kimura, Masami; Shimizu, Nobuyoshi
CORPORATE SOURCE:	Fac. Agric., Univ. Tokyo, Tokyo, 113, Japan
SOURCE:	Plant and Cell Physiology (1991), 32(6), 913-16 CODEN: PCPHA5; ISSN: 0032-0781
DOCUMENT TYPE:	Journal
LANGUAGE:	English

AB A synthetic oligonucleotide that corresponded to the consensus nucleotide sequence of the N-terminal region of mammalian metallothionein was used as a probe to isolate a cDNA clone from a soybean library. The clone had an open reading frame that encodes a protein of 79 amino acids which showed significant homol. to both N- and C-terminal regions of mammalian and Neurospora crassa metallothioneins.

IT **137630-14-9**, Protein (soybean clone 21-1-A 7.93-kilodalton reduced)
RL: PRP (Properties)
(amino acid sequence of)

L9 ANSWER 19 OF 531 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER:	1991:626378 CAPLUS
DOCUMENT NUMBER:	115:226378
TITLE:	Primary structure of molluskan metallothioneins deduced from PCR-amplified cDNA and mass spectrometry of purified proteins
AUTHOR(S):	Unger, Michael E.; Chen, Thomas T.; Murphy, Constance M.; Vestling, Martha M.; Fenselau, Catherine; Roesijadi, G.
CORPORATE SOURCE:	Chesapeake Biol. Lab., Univ. Maryland, Solomons, MD, 20688, USA
SOURCE:	Biochimica et Biophysica Acta (1991), 1074(3), 371-7 CODEN: BBACAQ; ISSN: 0006-3002
DOCUMENT TYPE:	Journal
LANGUAGE:	English

AB The primary structure of metallothioneins (MT) of a mollusk, the oyster Crassostrea virginica, was detd. by mol. cloning and mass spectrometry of

purified proteins. The cloning strategy included polymerase chain reaction (PCR) amplification of the responsible cDNAs from total cDNA using completely degenerate oligonucleotides (derived from the N-terminal amino acid sequence) and oligo(dT)20 as primers. Primer extension off mRNA was used as an independent detn. of the nucleotide sequence represented by the degenerate PCR primers. The deduced amino acid sequence was consistent with characteristics of class I MT. Twenty-one cysteine residues, were arranged in nine Cys-X-Cys motifs, five as Cys-Lys-Cys. A single Cys-X-X-Cys motif was also obsd. Two MTs that differ only in the presence or absence of an N-acetyl group exist in this organism. Masses of tryptic peptides of purified MTs corresponded with those of peptides predicted from tryptic cleavages of the deduced amino acid sequence. Allowing for known N-terminal modifications, 96% of the deduced sequence was confirmed by mass spectrometry. Comparison (FASTA algorithm) of the primary structure of the oyster MTs with those of other species indicated a higher similarity with vertebrate MTs than with those of other invertebrates.

IT **137086-78-3**, Metallothionein (Crassostrea virginica protein moiety reduced) **137086-79-4**, Metallothionein (Crassostrea virginica precursor protein moiety reduced)
RL: PRP (Properties)
(amino acid sequence of)

L9 ANSWER 20 OF 531 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1991:443096 CAPLUS
DOCUMENT NUMBER: 115:43096
TITLE: Multicopy CUP1 plasmids enhance cadmium and copper resistance levels in yeast
AUTHOR(S): Jeyaprakash, Ayyamperumal; Welch, Juliet W.; Fogel, Seymour
CORPORATE SOURCE: Dep. Plant Biol., Univ. California, Berkeley, CA, 94720, USA
SOURCE: Molecular and General Genetics (1991), 225(3), 363-8
CODEN: MGGEAE; ISSN: 0026-8925
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A 3.3 kb fragment of yeast genomic DNA was isolated by screening a genomic library constructed in the high copy no. 2-.mu.m plasmid YEp351 vector for clones capable of enhancing the degree of resistance of Saccharomyces cerevisiae strain MW3070-8B to cadmium. The insert contained 2 complete copies of the CUP1 gene open reading frame (183 bp), including the upstream promoter sequences (450 bp) with 2 conserved metal responsive cis-acting elements. Northern anal. showed that addn. of cadmium (0.02 .mu.M) or copper (50 .mu.M) to overnight liq. cultures of yeast induced expression of CUP1 transcripts from both chromosomal and plasmid-borne gene copies. The cloned 3.3 kb DNA in a high copy no. plasmid restored copper resistance to the sensitive strain LS70-3B.DELTA., deleted for the CUP1 gene (cup1.DELTA.), but failed to restore cadmium resistance. Thus, CUP1 gene expression in yeast appears to be influenced differently by cadmium and copper ions. Resistance to heavy metal poisoning resulted from enhanced gene product levels mediate cadmium and copper resistance; a higher gene product level was required to confer cadmium resistance.

IT **134801-80-2**, Metallothionein (Saccharomyces cerevisiae strain MW3070-8B gene CUP1 protein moiety reduced)
RL: PRP (Properties)
(amino acid sequence of)

L9 ANSWER 21 OF 531 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1991:443093 CAPLUS
DOCUMENT NUMBER: 115:43093
TITLE: Structure, spatial, and temporal expression of two sea urchin metallothionein genes, SpMTB1 and SpMTA

AUTHOR(S): Nemer, Martin; Thornton, Ruth D.; Stuebing, Elizabeth W.; Harlow, Patricia
CORPORATE SOURCE: Inst. Cancer Res., Fox Chase Cancer Cent., Philadelphia, PA, 19111, USA
SOURCE: Journal of Biological Chemistry (1991), 266(10), 6586-93
CODEN: JBCHA3; ISSN: 0021-9258
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The metallothionein-B genes of the sea urchin Strongylocentrotus purpuratus encode a metallothionein (MT) isoform distinguishable from the MTA isoform. The MTB subfamily consists of at least 2 genes, MTB1 and MTB2, and possibly 2-3 others. The unique MTB1 and MTA genes have a high degree of identity but diverge in structural detail and expression. Transcripts of the MTA, MTB1, troponin C Spec 1, and CyIIIa actin genes begin simultaneously to accumulate at an early blastula stage. MTB1 mRNA becomes localized in the embryonic gut and oral ectoderm, whereas MTA, Spec 1, and CyIIIa actin mRNAs are spatially restricted to the aboral ectoderm. Several DNA elements are localized at the same positions in the MTB1 and MTA genes: these include resp. CATA and TATA boxes, 2 metal response elements, and 3 distinct upstream DNA elements that are are also present, and in the same order, in the Spec 1 gene promoter. A heptameric sequence, element A, is present at 2 sites each in the Spec 1 and CyIIIa actin genes, 5 sites in MTA, but only 1 site in MTB1. Most strikingly, the first intron of MTA contains elements not found in the MTB1 introns, including a consensus metal response element, an element A, and the P3A site demonstrated in the CyIIIa actin genes to be linked to the regulation of spatial expression.

IT **107248-70-4**, Metallothionein (Strongylocentrotus purpuratus clone pMTb isoform B protein moiety reduced)
RL: PRP (Properties)
(amino acid sequence of)

L9 ANSWER 22 OF 531 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1991:241905 CAPLUS
DOCUMENT NUMBER: 114:241905
TITLE: Constitutive expression of the Saccharomyces cerevisiae CUP1 gene in Kluyveromyces lactis
AUTHOR(S): Macreadie, Ian G.; Horaitis, Ourania; Vaughan, Paul R.; Des Clark-Walker, G.
CORPORATE SOURCE: Div. Biomol. Eng., CSIRO, Parkville, 3052, Australia
SOURCE: Yeast (1991), 7(2), 127-35
CODEN: YESTE3; ISSN: 0749-503X
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Shuttle plasmids, pE1.CUP1B and pE1.CUP1E of 10.6 kb, have been constructed between the metallothionein-encoding CUP1 gene of Saccharomyces cerevisiae and a vector capable of replication in Kluyveromyces lactis. Introduction of these plasmids into K. lactis confers resistance to copper as well as to cadmium and silver. Resistance to these latter metal ions, in the absence of induction by copper, suggested that the CUP1 gene is constitutively expressed in the foreign background. Introduction of the lacZ reporter gene from Escherichia coli into a cloning site downstream from the CUP1 promoter showed that expression of this gene is constitutive in K. lactis but in S. cerevisiae induction by copper is necessary. Sequences upstream from the CUP1 promoter are involved in the constitutive expression since deletion of 91 nucleotides from this region abolishes metal resistance. It is suggested that a K. lactis protein, normally involved in activating transcription of the resident CUP1 gene in the presence of copper, can promote transcription in the absence of metal ion by binding to the upstream activation sequence of the introduced CUP1 gene.

IT **134117-40-1**, Metallothionein (Saccharomyces cerevisiae clone pE1.CUP1B gene CUP1 protein moiety reduced)
RL: PRP (Properties)
(amino acid sequence of)

L9 ANSWER 23 OF 531 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1993:596893 CAPLUS
DOCUMENT NUMBER: 119:196893
TITLE: Analysis of nucleotide sequence of the rightmost 43 kbp of herpesvirus saimiri (HVS) L-DNA: General conservation of genetic organization between HVS and Epstein-Barr virus
AUTHOR(S): Nicholas, John; Cameron, Keith R.; Coleman, Heather; Newman, Carol; Honess, Robert W.
CORPORATE SOURCE: Div. Virol., Natl. Inst. Med. Res., London, NW7 1AA, UK
SOURCE: Virology (1992), 188(1), 296-310
CODEN: VIRLAX; ISSN: 0042-6822
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The authors present an anal. of 43,658 bp of contiguous nucleotide sequence comprising the right terminal region (conventional orientation) of the unique protein-coding component (L-DNA) of the herpesvirus saimiri (HVS) genome. Within this region lie the genes encoding the 160-kDa virion protein, which is homologous to the 140-kDa membrane antigen of Epstein-Barr virus (EBV), thymidylate synthase (TS), and the immediate-early (IE) 52-kDa protein which is homologous to the EBV BMLF1 product. The 160-kDa gene of HVS lies at the right terminus of HVS L-DNA, its homolog in EBV occurring at the left terminus of the EBV genome (conventional orientation). The TS gene of HVS occurs within a group of 5 genes that have no homologs in EBV. The translation product of one of these genes, ECRF3, shows amino acid sequence and hydrophobicity pattern similarities to the HCMV and cellular G-protein-coupled receptor family of proteins. Another, ECLF2, is homologous to the cyclin family of cellular proteins. The 5 nonconserved genes lie adjacent to the 160-kDa gene. In EBV, the region of the right of the 140-kDa gene (BNRF1) contains the latent replication origin (OriP) and the open reading frames BCRF1, BWRF1 (repeated 12 times), BYRF1, BHLF1, and GHRF1, counterparts of which are not present in this position in HVS. The subsequent 18 genes in EBV (BFLF2 to BLRF2, approx. positions 56,000-89,500) are represented in HVS, and the relative positions and orientations of these genes are directly comparable between the two viruses. There then occurs a nonhomologous gene in HVS, and genes BLLF2 to BZLF1 (positions 89,500 to 103,200) in EBV which are not present in this region of HVS, before collinearity resumes. Thus, the HVS sequence presented here shows good collinearity between conserved genes in the right terminal region of HVS and the left terminal region of EBV and reveals the presence of two sets of unique genes which occur in exactly analogous positions in HVS and EBV.
IT **145717-32-4**, Protein (herpes saimiri virus gene ECLF1 reduced)
RL: PRP (Properties)
(amino acid sequence of)

L9 ANSWER 24 OF 531 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1993:464428 CAPLUS
DOCUMENT NUMBER: 119:64428
TITLE: Iron deficiency specific cDNA (Ids1) with two homologous cysteine rich MT domains from the roots of barley
AUTHOR(S): Okumura, Nami; Nishizawa, Naoko Kishi; Umehara, Yosuke; Ohata, Tomko; Mori, Satoshi
CORPORATE SOURCE: Lab. Plant Nutr. Fert., Univ. Tokyo, Tokyo, 113, Japan
SOURCE: Journal of Plant Nutrition (1992), 15(10), 2157-72

CODEN: JPNUDS; ISSN: 0190-4167
DOCUMENT TYPE: Journal
LANGUAGE: English
AB For the purpose of gene cloning for iron chelator mugineic acid (MA)-family phytosiderophores (HAs)-synthesis or Fe(III)-MAs transporter, a .delta.gt10 cDNA library was constructed from mRNA isolated from Fe-deficient barley roots. The library was then differentially screened between cDNA probes made from mRNA isolated from barley roots treated with +Fe and -Fe. Seven clones which hybridized specifically to the probe of Fe-deficiency were selected. Their inserts however were too short and not likely to include full-length mRNA. On the basis of these results, it was decided to screen a newly constructed .delta.zapII cDNA library with one of the 7 clones as a probe and a clone presumably having the full length of mRNA was selected. This clone was named Ids1. The sequenced Ids1 consists of 503 nucleotides contg. a putative open reading frame of 222 bp. It encodes a protein of 74 residues (7500 Da) having 2 cysteine-rich domains like animal metallothionein (class I MT).
IT **138672-77-2**, Protein (barley clone ids-1 7.46-kilodalton reduced)
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence of, complete)

L9 ANSWER 25 OF 531 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1993:421686 CAPLUS
DOCUMENT NUMBER: 119:21686
TITLE: Primary structure of the herpesvirus saimiri genome
AUTHOR(S): Albrecht, Jens Christian; Nicholas, John; Biller, Doris; Cameron, Keith R.; Biesinger, Brigitte; Newman, Carol; Wittmann, Sabine; Craxton, Molly A.; Coleman, Heather; et al.
CORPORATE SOURCE: Inst. Klin. Mol. Virol., Friedrich-Alexander Univ., Erlangen, D-8520, Germany
SOURCE: Journal of Virology (1992), 66(8), 5047-58
CODEN: JOVIAM; ISSN: 0022-538X
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The complete nucleotide sequence was detd. for the genome of herpesvirus saimiri, the prototype of gammaherpesvirus subgroup 2 (rhadinoviruses). The unique low-G+C-content DNA region has 112,930 bp with an av. base compn. of 34.5% G+C and is flanked by .apprx.35 noncoding high-G+C-content DNA repeats of 1444 bp (70.8% G+C) in tandem orientation. Seventy-six major open reading frames were identified, as well as a set of 7 U-RNA genes, for a total of 83 potential genes. The genes are closely arranged, with only a few regions of sizable noncoding sequences. For 60 of the predicted proteins, homologous sequences are found in other herpesviruses. Genes conserved between herpesvirus saimiri and Epstein-Barr virus (gammaherpesvirus subgroup 1) show that their genomes are generally collinear, although conserved gene blocks are sepd. by unique genes that appear to det. the particular phenotype of these viruses. Several deduced protein sequences of herpesvirus saimiri without counterparts in most of the other sequenced herpesviruses exhibited significant homol. with cellular proteins of known function. These include thymidylate synthase, dihydrofolate reductase, complement control proteins, the cell surface antigen CD59, cyclins, and G protein-coupled receptors. Searching for functional protein motifs revealed that the virus may encode a cytosine-specific methylase and a tyrosine-specific protein kinase. Several herpesvirus saimiri genes are potential candidates to cooperate with the gene for saimiri transformation-assocd. protein of subgroup A (STP-A) in T-lymphocyte growth stimulation.
IT **145717-32-4**, Protein (herpes saimiri virus gene ECLF1 reduced)
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(amino acid sequence of, complete)

L9 ANSWER 26 OF 531 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1993:402090 CAPLUS
DOCUMENT NUMBER: 119:2090
TITLE: Wheat Ec metallothionein genes. Like mammalian zinc(2+) metallothionein genes, wheat zinc(2+) metallothionein genes are conspicuously expressed during embryogenesis
AUTHOR(S): Kawashima, Ichiro; Kennedy, Theresa D.; Chino, Mitsuo; Lane, Byron G.
CORPORATE SOURCE: Fac. Agric., Univ. Tokyo, Japan
SOURCE: European Journal of Biochemistry (1992), 209(3), 971-6
CODEN: EJBCAI; ISSN: 0014-2956
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A cDNA library was prepd. from the bulk mRNA of mature wheat embryos and screened with mixed 32P-labeled oligonucleotide probes that encoded parts of the partial amino-acid sequence for the Zn-contg. Ec protein. Each DNA insert in 11 positives from a screen of 105 plaques encoded a 5' untranslated and a 3' untranslated region, in addn. to an open reading frame (of 81 amino acids) which, in every case, corresponded to at least 56 of the 59 amino acids in the polypeptide sequence previously detd. for the Ec protein. The three different mRNA sequences encoded in the cDNA probably correspond to single-copy genes in the A, B and D genomes of hexaploid wheat. A wheat genomic library was screened with 32P-labeled cDNA and gave a single pos. in a screen of 5 x 105 plaques. A 3.1-kb genomic fragment (gf-3.1) was sequenced and a cap site for the encoded mRNA was detd. by primer extension. The gf-3.1 sequences encodes an intronless mRNA for the Ec protein and contains appreciable amts. of 5' and 3' flanking sequences. In addn. to a putative TATA box, two inverted-repeat sequences and one direct-repeat sequence, the 5' flank in gf-3.1 contains a sequence similar to the abscisic-acid-responsive element in other higher-plant genes but does not contain sequences similar to the metal-responsive elements in animal metallothionein genes. Consistent with these findings, RNA blotting shows that accumulation of Ec mRNA is abundant in immature embryos, undetectable in germinated embryos and can be induced by adding abscisic acid, but not by adding Zn2+ to the medium in which mature wheat embryos are germinated. The findings suggest that the wheat Ec metallothionein genes, like mammalian liver metallothionein genes, are conspicuously expressed during embryogenesis.
IT **147955-31-5 147955-32-6**
RL: PRP (Properties); BIOL (Biological study)
(amino sequence of, complete)

L9 ANSWER 27 OF 531 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1993:402022 CAPLUS
DOCUMENT NUMBER: 119:2022
TITLE: Cloning and characterization of a gene involved in phytoene synthesis from tomato
AUTHOR(S): Ray, John; Moureau, Philippe; Bird, Colin; Bird, Alison; Grierson, Don; Maunders, Martin; Truesdale, Mark; Bramley, Peter; Schuch, Wolfgang
CORPORATE SOURCE: Plant Biotechnol., ICI Seeds, Bracknell, RG12 6EY, UK
SOURCE: Plant Molecular Biology (1992), 19(3), 401-4
CODEN: PMBIDB; ISSN: 0167-4412
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Tomato ripening is assocd. with a no. of physiol. and biochem. changes including degrdn. of chlorophyll in the plastids of the ripening tomato fruit and synthesis of lycopene, which is responsible for the red color of ripe fruit. Previously the authors cloned the mRNAs for at least 19

proteins whose expression is increased during ripening, and investigated their function using antisense RNA. This led to the identification of pTOM5, a ripening-specific cDNA clone (M. J. Maunders et al., 1987), as encoding an enzyme crit. in carotenoid biosynthesis. Here the cloning and characterization of genomic sequences with homol. to pTOM5 is reported. Two loci homologous to pTOM5 were sequenced. One locus represents a pseudogene.

IT **147994-68-1**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence of, complete)

L9 ANSWER 28 OF 531 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1993:162460 CAPLUS
DOCUMENT NUMBER: 118:162460
TITLE: Keratinocyte or epithelial cell line expressing the human papillomavirus E5 gene
INVENTOR(S): Dimaio, Daniel C.; Dotto, Gian Paolo
PATENT ASSIGNEE(S): Yale University, USA
SOURCE: PCT Int. Appl., 46 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9220784	A1	19921126	WO 1991-US6039	19910823
W: CA, JP				
RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LU, NL, SE				
PRIORITY APPLN. INFO.:			US 1991-701413	19910516

AB The title cell lines are developed for use in drug screening to identify compds. that inhibit the action of the E5 transforming gene. A DNA fragment contg. the E5 gene from either bovine papillomavirus (BPV) or human papillomavirus type 16 (HPV16) was inserted into retroviral vector pLXSN, and plasmids contg. the vectors were transfected into ecotropic packing cell line .gamma.cre. The BPV gene cloned in .gamma.cre cells, was expressed in C127 murine mammary carcinoma fibroblasts as shown by E5 RNA and protein formation and foci of morphol. transformed cells in vitro, and induced tumors in nude mice injected with BPV-infected C127 cells or p117 mouse keratinocytes. Since .gamma.cre cells produced low titers of HPV16, this virus was cloned in amphotropic packaging cell line PA317; HPV16 gene E5 (sequence given) was expressed (E5 RNA formation) in both NIH 3T3 fibroblasts and p117 cells, and HPV16 was tumorigenic in p117 keratinocytes but not in NIH 3T3 fibroblasts.

IT **114572-74-6**, Protein (human papilloma virus 16 gene E5 reduced)
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence of, complete, neoplastic transformation in relation to)

L9 ANSWER 29 OF 531 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1993:117798 CAPLUS
DOCUMENT NUMBER: 118:117798
TITLE: The phylogenetic relationship and complete nucleotide sequence of human papillomavirus type 35
AUTHOR(S): Marich, James E.; Pontsler, Aaron V.; Rice, Sallie M.; McGraw, Kathy A.; Dubensky, Thomas W.
CORPORATE SOURCE: Syngene Inc., San Diego, CA, 92121, USA
SOURCE: Virology (1992), 186(2), 770-6
CODEN: VIRLAX; ISSN: 0042-6822

DOCUMENT TYPE: Journal
LANGUAGE: English
AB The 7851-bp nucleotide sequence of human papillomavirus (HPV) type 35 was detd. HPV 35 is assocd. with high-grade cervical intraepithelial neoplasia and invasive carcinomas. From the HPV 35 sequence, open reading frames encoding putative proteins E6, E7, E1, E2, E4, E5, L2, and L1, common to other mucosal HPV types, were identified. Structural and control elements present in the long control region (LCR) conserved among other mucosal HPV types were also present in HPV 35. Anal. of the LCR revealed an addnl. 20-bp sequence element present in all HPV types assocd. with malignant proliferation. To further classify HPV 35 with regard to oncogenic potential, phylogenic anal. of the E6 and E7 proteins from the anogenital HPV types 6, 11, 16, 18, 31, 35, 39, 43, 44, 45, and 51 was performed. This anal. indicated 3 distinct HPV subgroups; those assocd. with benign lesions and 2 branches of those HPV types more often assocd. with malignant proliferation. HPV 35 is most closely related to HPV types 31 and 16.
IT **146313-57-7**, Protein (human papilloma virus 35 gene E5)
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence of, complete)

L9 ANSWER 30 OF 531 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1993:74537 CAPLUS
DOCUMENT NUMBER: 118:74537
TITLE: Herpesvirus saimiri encodes homologs of G protein-coupled receptors and cyclins
AUTHOR(S): Nicholas, John; Cameron, Keith R.; Honess, Robert W.
CORPORATE SOURCE: Div. Virol., Natl. Inst. Med. Res., London, NW7 1AA, UK
SOURCE: Nature (London, United Kingdom) (1992), 355(6358), 362-5
CODEN: NATUAS; ISSN: 0028-0836
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Two genes, have been identified which occur in a region of divergence between herpes virus saimiri (HVS) and Epstein-Barr virus (EBV), that have cellular homologs. One of these, ECRF3, is homologous to the genes encoding the human cytomegalovirus (HCMV) and cellular G protein-coupled receptor family of proteins. The other HVS gene, ECLF2, is homologous to the genes encoding cellular cyclins and is the first reported example of a viral cyclin. The presence of G protein-coupled receptor and cyclin homologs in HVS suggests that these genes may be important in the regulation of viral and cellular processes during productive and/or latent infection of host cells, and in particular may be of relevance in the transformation and rapid proliferation of T cells during HVS infections of hosts susceptible to HVS-induced lymphoproliferative diseases.
IT **145717-32-4**, Protein (herpes saimiri virus gene ECLF1 reduced)
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence of, complete)

=> fil reg; s 145717-32-4 or 146313-57-7 or 114572-74-6 or 147994-68-1 or 147955-31-5 or 147955-32-6
FILE 'REGISTRY' ENTERED AT 14:27:52 ON 09 AUG 2004
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STRUCTURE FILE UPDATES: 8 AUG 2004 HIGHEST RN 724421-42-5
DICTIONARY FILE UPDATES: 8 AUG 2004 HIGHEST RN 724421-42-5

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http://www.cas.org/ONLINE/DBSS/registryss.html

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             1 145717-32-4
               (145717-32-4/RN)
             1 146313-57-7
               (146313-57-7/RN)
             1 114572-74-6
               (114572-74-6/RN)
             1 147994-68-1
               (147994-68-1/RN)
             1 147955-31-5
               (147955-31-5/RN)
             1 147955-32-6
               (147955-32-6/RN)
L10          6 145717-32-4 OR  146313-57-7 OR  114572-74-6 OR  147994-68-1 OR
               147955-31-5 OR 147955-32-6
```

Registry numbers for hit Registry numbers

```
=> s  138672-77-2 or  134117-40-1 or  107248-70-4 or  134801-80-2 or 137086-78-3 or
137086-79-4 or  137630-14-9

             1 138672-77-2
               (138672-77-2/RN)
             1 134117-40-1
               (134117-40-1/RN)
             1 107248-70-4
               (107248-70-4/RN)
             1 134801-80-2
               (134801-80-2/RN)
             1 137086-78-3
               (137086-78-3/RN)
             1 137086-79-4
               (137086-79-4/RN)
             1 137630-14-9
               (137630-14-9/RN)
L11          7 138672-77-2 OR  134117-40-1 OR  107248-70-4 OR  134801-80-2 OR
               137086-78-3 OR  137086-79-4 OR  137630-14-9

=> s  138672-78-3 or  143972-11-6 or  143972-14-9 or  143972-16-1 or  128392-85-8 or
128825-82-1 or  109189-62-0

             1 138672-78-3
               (138672-78-3/RN)
             1 143972-11-6
               (143972-11-6/RN)
             1 143972-14-9
               (143972-14-9/RN)
             1 143972-16-1
```

```
                (143972-16-1/RN)
             1 128392-85-8
                (128392-85-8/RN)
             1 128825-82-1
                (128825-82-1/RN)
             1 109189-62-0
                (109189-62-0/RN)
L12          7 138672-78-3 OR  143972-11-6 OR  143972-14-9 OR  143972-16-1 OR
               128392-85-8 OR  128825-82-1 OR  109189-62-0

=> s  125691-65-8 or  98513-00-9 or  128392-65-4 or  114572-74-6 or  111694-22-5 or
114541-20-7

             1 125691-65-8
                (125691-65-8/RN)
             1 98513-00-9
                (98513-00-9/RN)
             1 128392-65-4
                (128392-65-4/RN)
             1 114572-74-6
                (114572-74-6/RN)
             1 111694-22-5
                (111694-22-5/RN)
             1 114541-20-7
                (114541-20-7/RN)
L13          6 125691-65-8 OR  98513-00-9 OR  128392-65-4 OR  114572-74-6 OR
               111694-22-5 OR  114541-20-7

=> s l10-l13
L14         25 (L10 OR L11 OR L12 OR L13)


=> s l14 and l2
L15         25 L14 AND L2

=> d cn rn sql kwic nte l15 1-25; fil hom

L15  ANSWER 1 OF 25  REGISTRY  COPYRIGHT 2004 ACS on STN
CN   Synthetase, phytoene (tomato clone GTOM5 reduced) (9CI)  (CA INDEX NAME)
RN   147994-68-1  REGISTRY
SQL  412
SEQ    351 ASRFPVWASL VLYRKILDEI EANDYNNFTK RAYVSKSKQV DCITYCICKI

       401 SCASYKTASL QR
HITS AT:   392-402

**RELATED SEQUENCES AVAILABLE WITH SEQLINK**

L15  ANSWER 2 OF 25  REGISTRY  COPYRIGHT 2004 ACS on STN
CN   Metallothionein II (wheat clone cDNA-II reduced) (9CI)  (CA INDEX NAME)
RN   147955-32-6  REGISTRY
SQL  81

SEQ      1 MGCDDKCGCA VPCPGGTGCR CTSARSGAAA GEHTTCGCGE HCGCNPCACG
HITS AT:   3-13

**RELATED SEQUENCES AVAILABLE WITH SEQLINK**

L15  ANSWER 3 OF 25  REGISTRY  COPYRIGHT 2004 ACS on STN
```

use Registry # to match sequence to citation

Sequence Length

CN Metallothionein II (wheat clone cDNA-III reduced) (9CI) (CA INDEX NAME)
RN **147955-31-5** REGISTRY
SQL 81

SEQ 1 MGCNDKCGCA VPCPGGTGCR CTSARSDAAA GEHTTCGCGE HCGCNPCACG
======== ===
HITS AT: 3-13

RELATED SEQUENCES AVAILABLE WITH SEQLINK

L15 ANSWER 4 OF 25 REGISTRY COPYRIGHT 2004 ACS on STN
CN Protein (human papillomavirus 35 gene E5) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Protein (human papilloma virus 35 gene E5)
RN **146313-57-7** REGISTRY
SQL 81

SEQ 1 MIDLTASSTV LLCFLLCFCV LLCLCLLVRS LLLSVSLYSA LILLVLILWV
======== ===
HITS AT: 13-23

RELATED SEQUENCES AVAILABLE WITH SEQLINK

L15 ANSWER 5 OF 25 REGISTRY COPYRIGHT 2004 ACS on STN
CN Protein (saimiriine herpesvirus gene ECLF1 reduced) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Protein (herpes saimiri virus gene ECLF1 reduced)
RN **145717-32-4** REGISTRY
SQL 407

SEQ 1 MAPRRRKAKR RRHTLRSECK DKCKCHVQCY VSPRKRRRKL KPQGDDDINT
== =========
HITS AT: 19-29

RELATED SEQUENCES AVAILABLE WITH SEQLINK

L15 ANSWER 6 OF 25 REGISTRY COPYRIGHT 2004 ACS on STN
CN Protein (barley clone pB22E.g411/pB22E.g312/pB22E.g1 gene B22E reduced) (9CI) (CA INDEX NAME)
RN **143972-16-1** REGISTRY
SQL 119

SEQ 1 MSCCGGKCGC GAGCQCGTGC GGCKMFPDVE ATAGAAAMVM PTASHKGSSG
======= ==========
HITS AT: 4-20

L15 ANSWER 7 OF 25 REGISTRY COPYRIGHT 2004 ACS on STN
CN Protein (barley clone pB22E.g49 gene B22EL8 reduced) (9CI) (CA INDEX NAME)
RN **143972-14-9** REGISTRY
SQL 115

SEQ 1 MSCCGGKCGC GAGCQCGTGC GGCKMFPDVE ATAGAAAMVM PTASHKGSSG
======= ==========
HITS AT: 4-20

L15 ANSWER 8 OF 25 REGISTRY COPYRIGHT 2004 ACS on STN
CN Protein (barley clone pB22EL8 gene B22EL8 reduced) (9CI) (CA INDEX NAME)
RN **143972-11-6** REGISTRY
SQL 115

SEQ 1 MSCCGGKCGC GAGCQCGTGC GGCKMFPDVE ATAGAAAMVM PTASHKGSSG

```
                ======= ==========
HITS AT:    4-20

**RELATED SEQUENCES AVAILABLE WITH SEQLINK**

L15  ANSWER 9 OF 25  REGISTRY  COPYRIGHT 2004 ACS on STN
CN   Protein (corn clone pCIB1324 7.48-kilodalton reduced) (9CI)  (CA INDEX
     NAME)
OTHER NAMES:
CN   Metallothionein (corn clone pCIB1325 protein moiety reduced)
CN   Protein (corn clone pZSS6 metallothionein-like)
RN   138672-78-3  REGISTRY
SQL  76

SEQ       1 MSCSCGSSCG CGSSCKCGKK YPDLEETSTA AQPTVVLGVA PEKKAAPEFV
                ====== =====
HITS AT:    5-15

**RELATED SEQUENCES AVAILABLE WITH SEQLINK**

L15  ANSWER 10 OF 25  REGISTRY  COPYRIGHT 2004 ACS on STN
CN   Protein (barley clone ids-1 7.46-kilodalton reduced) (9CI)  (CA INDEX
     NAME)
RN   138672-77-2  REGISTRY
SQL  74

SEQ       1 MSCSCGSSCG CGSNCNCGKM YPDLEEKSGA TMQVTVIVLG VGSAKVQFEE
                ====== =====
HITS AT:    5-15

**RELATED SEQUENCES AVAILABLE WITH SEQLINK**

L15  ANSWER 11 OF 25  REGISTRY  COPYRIGHT 2004 ACS on STN
CN   Protein (soybean clone 21-1-A 7.93-kilodalton reduced) (9CI)  (CA INDEX
     NAME)
RN   137630-14-9  REGISTRY
SQL  79

SEQ       1 MSCCGGNCGC GSSCKCGNGC GGCKMYPDLS YTESTTTETL VMGVAPVKAQ
              ======= ==========
HITS AT:    4-20

**RELATED SEQUENCES AVAILABLE WITH SEQLINK**

L15  ANSWER 12 OF 25  REGISTRY  COPYRIGHT 2004 ACS on STN
CN   Metallothionein (Crassostrea virginica precursor protein moiety reduced)
     (9CI)  (CA INDEX NAME)
RN   137086-79-4  REGISTRY
SQL  75

SEQ       1 MSDPCNCIET GTCACSDSCP ATGCKCGPGC KCGDDCKCAG CKVKCSCTSE
                                        ===== ======
HITS AT:    26-36

**RELATED SEQUENCES AVAILABLE WITH SEQLINK**

L15  ANSWER 13 OF 25  REGISTRY  COPYRIGHT 2004 ACS on STN
CN   Metallothionein (Crassostrea virginica protein moiety reduced) (9CI)  (CA
     INDEX NAME)
RN   137086-78-3  REGISTRY
SQL  74
```

```
SEQ      1 SDPCNCIETG TCACSDSCPA TGCKCGPGCK CGDDCKCAGC KVKCSCTSEG
                                   ====== =====
HITS AT:   25-35

L15  ANSWER 14 OF 25  REGISTRY  COPYRIGHT 2004 ACS on STN
CN   Metallothionein (Saccharomyces cerevisiae strain MW3070-8B gene CUP1
     protein moiety reduced) (9CI)  (CA INDEX NAME)
RN   134801-80-2  REGISTRY
SQL  61

SEQ      1 MFSELINFQN EGHECQCQCG SCKNNEQCQK SCSCPTGCNS DDKCPCGNKS
                                     === ========
HITS AT:   28-38

**RELATED SEQUENCES AVAILABLE WITH SEQLINK**

L15  ANSWER 15 OF 25  REGISTRY  COPYRIGHT 2004 ACS on STN
CN   Metallothionein (Saccharomyces cerevisiae clone pE1.CUP1B gene CUP1
     protein moiety reduced) (9CI)  (CA INDEX NAME)
RN   134117-40-1  REGISTRY
SQL  70

SEQ      1 MFSELDPQLS TAEFINFQNE GHECQCQCGS CKNNEQCQKS CSCPTGCNSD
                                               ==== =======
HITS AT:   37-47

L15  ANSWER 16 OF 25  REGISTRY  COPYRIGHT 2004 ACS on STN
CN   Metallothionein (Mimulus guttatus clone J49 protein moiety reduced) (9CI)
     (CA INDEX NAME)
RN   128825-82-1  REGISTRY
SQL  72

SEQ      1 MSSGCSCGSG CKCGDNCSCS MYPDMETNTT VTMIEGVAPL KMYSEGSEKS
               ==== =======
HITS AT:   7-17

L15  ANSWER 17 OF 25  REGISTRY  COPYRIGHT 2004 ACS on STN
CN   Metallothionein (pea strain Feltham First gene PsMTA protein moiety
     reduced) (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN   GenBank CAA80645
CN   GenBank CAA80645 (Translated from: GenBank Z23097)
CN   Metallothionein (pea gene PsMTA protein moiety reduced)
CN   Protein (pea gene PsMTA metallothionein-like)
RN   128392-85-8  REGISTRY
SQL  75

SEQ      1 MSGCGCGSSC NCGDSCKCNK RSSGLSYSEM ETTETVILGV GPAKIQFEGA
              ===== ======
HITS AT:   6-16

**RELATED SEQUENCES AVAILABLE WITH SEQLINK**

L15  ANSWER 18 OF 25  REGISTRY  COPYRIGHT 2004 ACS on STN
CN   Metallothionein (Strongylocentrotus purpuratus clone .lambda.MT206 protein
     moiety reduced) (9CI)  (CA INDEX NAME)
RN   128392-65-4  REGISTRY
SQL  64

SEQ      1 MPDVKCVCCK EGKECACFGQ DCCKTGECCK DGTCCGICTN AACKCANGCK
                                                       ======
        51 CGSGCSCTEG NCAC
```

```
            =====
HITS AT:    45-55

**RELATED SEQUENCES AVAILABLE WITH SEQLINK**

L15  ANSWER 19 OF 25  REGISTRY  COPYRIGHT 2004 ACS on STN
CN   Metallothionein I (Candida glabrata strain 67 protein moiety reduced)
     (9CI)  (CA INDEX NAME)
RN   125691-65-8  REGISTRY
SQL  63

SEQ      1 MANDCKCPNG CSCPNCANGG CQCGDKCECK KQSCHGCGEQ CKCGSHGSSC
                                                                 =
        51 HGSCGCGDKC DCK
           ==========
HITS AT:    50-60

L15  ANSWER 20 OF 25  REGISTRY  COPYRIGHT 2004 ACS on STN
CN   Protein (human papillomavirus 16 gene E5 reduced) (9CI)  (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN   Protein (human papilloma virus 16 gene E5 reduced)
OTHER NAMES:
CN   29: PN: WO0141799 PAGE: 20 claimed sequence
CN   E5 protein (human papillomavirus 16 isolate OR5110 gene E5)
CN   Protein E5 (human papillomavirus 16)
RN   114572-74-6  REGISTRY
SQL  83

SEQ      1 MTNLDTASTT LLACFLLCFC VLLCVCLLIR PLLLSVSTYT SLIILVLLLW
                       ======= ====
HITS AT:    14-24

**RELATED SEQUENCES AVAILABLE WITH SEQLINK**

L15  ANSWER 21 OF 25  REGISTRY  COPYRIGHT 2004 ACS on STN
CN   Protein (tomato clone pTOM5 46.7-kilodalton reduced) (9CI)  (CA INDEX
     NAME)
RN   114541-20-7  REGISTRY
SQL  412

SEQ    351 ASRFPVWASL VLYRKILDEI EANDYNNFTK RAYVSKSKQV DCITYCICKI
                                                    =========
       401 SCASYKNASL QR
           ==
HITS AT:    392-402

**RELATED SEQUENCES AVAILABLE WITH SEQLINK**

L15  ANSWER 22 OF 25  REGISTRY  COPYRIGHT 2004 ACS on STN
CN   Metallothionein (Lytechinus pictus clone 15C9 protein moiety reduced)
     (9CI)  (CA INDEX NAME)
RN   111694-22-5  REGISTRY
SQL  68

SEQ      1 MPGPDVKCFC CQDGKQCACG GGECCITGKC CQEGDGTCCG KCSNAACKCA
                                                             ==
        51 DGCKCEGACA CTMGNCTC
           =========
HITS AT:    49-59

L15  ANSWER 23 OF 25  REGISTRY  COPYRIGHT 2004 ACS on STN
CN   Metallothionein (Drosophila melanogaster clone pCd2/pCd14 protein moiety
```

reduced) (9CI) (CA INDEX NAME)
RN **109189-62-0** REGISTRY
SQL 43

SEQ 1 MVCKGCGTNC QCSAQKCGDN CACNKDCQCV CKNGPKDQCC SNK
==== =======
HITS AT: 17-27

RELATED SEQUENCES AVAILABLE WITH SEQLINK

L15 ANSWER 24 OF 25 REGISTRY COPYRIGHT 2004 ACS on STN
CN Metallothionein (Strongylocentrotus purpuratus clone pMTb isoform B protein moiety reduced) (9CI) (CA INDEX NAME)
RN **107248-70-4** REGISTRY
SQL 65

SEQ 1 MPDVKCVCCK EGNECACTGQ DCCTIGKCCK DGTCCGKCSN AACKTCADGC
=====
51 TCGSGCSCTE GNCPC
======
HITS AT: 46-56

RELATED SEQUENCES AVAILABLE WITH SEQLINK

L15 ANSWER 25 OF 25 REGISTRY COPYRIGHT 2004 ACS on STN
CN Metallothionein (Strongylocentrotus purpuratus protein moiety reduced) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN Metallothionein A (Strongylocentrotus purpuratus synthetic gene-encoded)
RN **98513-00-9** REGISTRY
SQL 64

SEQ 1 MPDVKCVCCT EGKECACFGQ DCCVTGECCK DGTCCGICTN AACKCANGCK
======
51 CGSGCSCTEG NCAC
=====
HITS AT: 45-55

RELATED SEQUENCES AVAILABLE WITH SEQLINK

FILE 'HOME' ENTERED AT 14:29:40 ON 09 AUG 2004